**WHAT IS CLAIMED IS:**

1. A process for producing carotenoids comprising cultivating in a culture medium a recombinant organism containing a gene for one or more active oxygen species-quenching factor that is disrupted with a disruption cassette specific to the gene, and recovering carotenoids from the culture.

2. A process according to claim 1 wherein the recombinant organism belongs to the kingdom of *Monera, Protista or Fungi*.

3. A process according to claim 1 wherein the recombinant organism belongs to a genus selected from the group consisting of *Erwinia, Rhodobacter, Myxococcus, Flavobacter, Paracoccus, Synechococcus, Synechocystis, Agrobacterium, Streptomyces, Haematococcus, Dunaliella, Phaffia, Xanthophyllomyces, Neurospora, Rhodotorula, Blakeslea,* and *Phycomyces*.

4. A process according to claim 3 wherein the recombinant organism is a strain of *P. rhodozyma*.

5. A process according to claim 4 wherein the recombinant organism is *P. rhodozyma* ATCC 96594.

6. A process according to claim 1 wherein the active oxygen species-quenching factor is selected from the group consisting of mitochondrial superoxide dismutase (SOD), cytoplasmic superoxide dismutase (SOD), catalase, and combinations thereof.

7. A process according to claim 1 wherein the active oxygen species-quenching factors are encoded by a polynucleotide selected from the group consisting of SEQ ID NOs:1, 2, 3, 4, 6, and 8.

8. A recombinant organism for producing carotenoids comprising a gene for at least one active oxygen species-quenching factor, which gene is substantially disrupted with a disruption cassette specific to the gene.

9. A recombinant organism according to claim 8 wherein the recombinant organism belongs to the kingdom of *Monera, Protista or Fungi*.

10. A recombinant organism according to claim 9 wherein the recombinant organism belongs to a genus selected from the group consisting of *Erwinia, Rhodobacter, Myxococcus, Flavobacter, Paracoccus, Synechococcus, Synechocystis, Agrobacterium, Streptomyces, Haematococcus, Dunaliella, Phaffia, Xanthophyllomyces, Neurospora, Rhodotorula, Blakeslea,* and *Phycomyces*.

11. A recombinant organism according to claim 8 wherein the active oxygen species-quenching factor to be disrupted is selected from the group consisting of mitochondrial superoxide dismutase (SOD), cytoplasmic superoxide dismutase (SOD), catalase, and combinations thereof.

12. A disruption cassette for disrupting a gene coding for an active oxygen species-quenching factor effective in carotenogenesis in a carotenogenic organism comprising a nucleotide sequence that codes for an active oxygen species-quenching factor that is substantially identical to a part of a DNA sequence coding for an active oxygen species-quenching factor and a selectable marker gene.

13. A disruption cassette according to claim 12 wherein the organism belongs to the kingdom of *Monera, Protista or Fungi*.

14. A disruption cassette according to claim 13 wherein the organism belongs to a genus selected from the group consisting of *Erwinia, Rhodobacter, Myxococcus, Flavobacter, Paracoccus, Synechococcus, Synechocystis, Agrobacterium, Streptomyces, Haematococcus, Dunaliella, Phaffia, Xanthophyllomyces, Neurospora, Rhodotorula, Blakeslea,* and *Phycomyces*.

15. A disruption cassette according to claim 12 wherein the active oxygen species-quenching factor to be disrupted is selected from the group consisting of mitochondrial superoxide dismutase (SOD), cytoplasmic superoxide dismutase (SOD), catalase, and combinations thereof.

16. A disruption cassette according to claim 12 wherein the nucleotide sequence coding for an active oxygen species-quenching factor is identical to at least a part of a polynucleotide sequence coding for the active oxygen species-quenching factor of the organism into which the disruption cassette is to be introduced.

17. A disruption cassette according to claim 16 wherein the nucleotide sequence that codes for an active oxygen species-quenching factor, and that is identical to a part of the polynucleotide coding for an active oxygen species-quenching factor comprises a deletion and/or mutation compared to the corresponding functional gene.

18. A recombinant DNA sequence coding for an active oxygen species-quenching factor effective in carotenogenesis in a carotenogenic organism.

19. A recombinant DNA sequence according to claim 18, wherein the organism belongs to the kingdom of *Monera, Protista or Fungi*.

20. A recombinant DNA sequence according to claim 19 wherein the organism belongs to the kingdom of *Monera, Protista or Fungi*.

21. A recombinant DNA sequence according to claim 20 wherein the organism belongs to a genus selected from the group consisting of *Erwinia, Rhodobacter,*

*Myxococcus, Flavobacter, Paracoccus, Synechococcus, Synechocystis, Agrobacterium, Streptomyces, Haematococcus, Dunaliella, Phaffia, Xanthophyllomyces Neurospora, Rhodotorula, Blakeslea,* and *Phycomyces*.

22. A recombinant DNA sequence according to claim 18 wherein the recombinant DNA sequence is isolated from a microorganism of *P. rhodozyma*.

23. A recombinant DNA sequence according to claim 22 wherein the microorganism is *P. rhodozyma* ATCC 96594.

24. A recombinant DNA sequence according to claim 18 wherein the active oxygen species-quenching factor is a mitochondrial superoxide dismutase.

25. A recombinant DNA sequence according to claim 24 wherein the mitochondrial superoxide dismutase is encoded by a polynucleotide sequence identified by SEQ ID NO: 1 or 4.

26. A recombinant DNA sequence according to claim 25 wherein the mitochondrial superoxide dismutase is encoded by a polynucleotide sequence that binds under high stringency conditions to the sequence of SEQ ID NO: 1 or 4, and has a mitochondrial superoxide dismutase activity.

27. A recombinant DNA sequence according to claim 18 wherein the active oxygen species-quenching factor is cytoplasmic superoxide dismutase.

28. A recombinant DNA sequence according to claim 27 wherein the cytoplasmic superoxide dismutase is encoded by a polynucleotide sequence identified by SEQ ID NO: 2 or 6.

29. A recombinant DNA sequence according to claim 28 wherein the cytoplasmic superoxide dismutase is encoded by a polynucleotide sequence that binds under high stringency conditions to the sequence of SEQ ID NO: 2 or 6, and has a cytoplasmic superoxide dismutase activity.

30. A recombinant DNA sequence according to claim 18 wherein the active oxygen species-quenching factor is catalase.

31. A recombinant DNA sequence according to claim 30 wherein the catalase is encoded by a polynucleotide sequence identified by SEQ ID NO: 3 or 8.

32. A recombinant DNA sequence according to claim 31 wherein the catalase is encoded by a polynucleotide sequence that binds under high stringency conditions to the sequence of SEQ ID NO: 3 or 8, and has catalase activity.

33. A recombinant DNA fragment comprising a coding region for a transit peptide upstream of the coding region of an objective protein.

34. A recombinant DNA fragment according to claim 33 wherein the objective protein is mitochondrial superoxide dismutase.

35. A method for locating an objective protein in mitochondria comprising expressing the recombinant DNA fragment of claim 24 or 25 in a recombinant host organism.

36. A method for cloning a gene encoding an active oxygen species-quenching factor effective in carotenogenesis in a carotenogenic organism comprising providing as a probe or primer a polynucleotide sequence encoding a polypeptide having the activity of a

mitochondrial superoxide dismutase (SOD), a cytoplasmic superoxide dismutase (SOD) and/or a catalase.

37. A method according to claim 36 wherein the polynucleotide sequence is selected from the group consisting of SEQ ID NOs:1, 2, 3, 4, 6, 8, and fragments thereof.